

SEQUENCE LISTING



<110> French, Cynthia K.
Schneider, Patrick A.
Yamamoto, Karen K.

<120> Prostate Cancer-Specific Marker

<130> 107-206US-C

<140> 09/680,121
<141> 2000-10-04

<150> 60/041,246
<151> 1997-03-07

<150> 60/047,811
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<170> PatentIn Ver. 2.1

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cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174
Met Ala Pro Ile Thr Thr Ser Arg

gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt			222
Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe			
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ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga			270
Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg			
25	30	35	40
aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg			318
Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val			
45	50	55	
ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag			366
Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys			
60	65	70	
ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca			414
Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro			
75	80	85	
aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat			462
Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn			
90	95	100	
ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat			510
Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn			
105	110	115	120
gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct			558
Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro			
125	130	135	
gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag			606
Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu			
140	145	150	
aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa			654
Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys			
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gca ttt gtg gtc aat atc aag gaa gcc cgt ggc ttg cca gcc atg gat			702
Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp			
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gag cag tcg atg acc tct gac cca tat atc aaa atg acg atc ctc cca			750
Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro			

185	190	195	200	
gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat				798
Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp				
205	210	215		
cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa				846
Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln				
220	225	230		
atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt				894
Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe				
235	240	245		
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Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile				
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Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg				
265	270	275	280	
aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc				1038
Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys				
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tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga				1086
Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg				
300	305	310		
cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa				1134
His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys				
315	320	325		
gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat				1182
Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Thr His				
330	335	340		
gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt				1230
Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe				
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gat att cct tgt gag ggc ctt gaa gat ata agt gtt gaa ttt ttg gtt				1278
Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val				
365	370	375		
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Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val				

380

385

390

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Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
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Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
410 415 420

ggc tagcatccta gccgtgagtt ggaacttaaa ggttttact aggcaaggag 1475
Gly
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<213> Homo sapiens

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20 25 30

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
35 40 45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
50 55 60

Glu Asn Leu Asn Ser Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
65 70 75 80

Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
85 90 95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
100 105 110

Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
115 120 125

Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
130 135 140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
145 150 155 160

Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
165 170 175

Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
195 200 205

Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr

210

215

220

Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
225 230 235 240

Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
245 250 255

Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
260 265 270

Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg
275 280 285

Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
290 295 300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
305 310 315 320

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
325 330 335

Arg Ile Ser Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
340 345 350

Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
355 360 365

Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
370 375 380

Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
385 390 395 400

Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile
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Ala Lys Trp His Val Leu Cys Asp Gly
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<213> rat

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Phe Ala Trp Ile Cys Cys Gln Arg Arg Ser Ala Lys Ser Asn Lys Thr
35 40 45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
50 55 60

Glu Asn Leu Ser Ser Lys Lys Phe Gly Gly Asp Asp Lys Ser Glu
65 70 75 80

Ala Lys Arg Lys Ala Ala Leu Pro Asn Leu Ser Leu His Leu Asp Leu

85

90

95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Pro Lys Ala
100 105 110

Gly Ser Ser Ser Asp Leu Glu Asn Val Thr Pro Lys Leu Phe Pro Glu
115 120 125

Thr Glu Lys Glu Ala Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
130 135 140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Leu Ser
145 150 155 160

Leu Glu Tyr Asn Phe Glu Lys Lys Ala Phe Val Val Asn Ile Lys Glu
165 170 175

Ala Gln Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
195 200 205

Arg Val Leu Arg Lys Thr Leu Asp Pro Val Phe Asp Glu Thr Phe Thr
210 215 220

Phe Tyr Gly Val Pro Tyr Pro His Ile Gln Glu Leu Ser Leu His Phe
225 230 235 240

Thr Val Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Val Ile Gly Glu
245 250 255

Val Leu Val Pro Leu Ser Gly Ile Glu Leu Ser Asp Gly Lys Met Leu
260 265 270

Met Thr Arg Glu Ile Ile Lys Arg Asn Ala Lys Lys Ser Ser Gly Arg
275 280 285

Gly Glu Leu Leu Val Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
290 295 300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
305 310 315 320

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
325 330 335

Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala

340

345

350

Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Ser Leu Glu
355 360 365

Glu Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
370 375 380

Asn Glu Val Ile Gly Arg Leu Val Leu Gly Ala Thr Ala Glu Gly Ser
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Gly Gly Gly His Trp Lys Glu Ile Cys Asp Phe Pro Arg Arg Gln Ile
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Ala Lys Trp His Met Leu Cys Asp Gly
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<211> 117

<212> PRT

<213> Homo sapiens

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<221> PEPTIDE

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<223> PKC-C2 internal repeat (amino acid positions
154-271)

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Arg Ile Tyr Leu Glu Ile Asn Val Lys Glu Asn Leu Leu Thr Val Gln
20 25 30

Ile Lys Glu Gly Arg Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser
35 40 45

Asp Pro Tyr Val Lys Val Lys Leu Ile Pro Asp Asp Lys Asp Gln Ser
50 55 60

Lys Lys Lys Thr Arg Thr Thr Lys Ala Cys Leu Asn Pro Val Trp Asn
65 70 75 80

Glu Thr Leu Thr Tyr Asp Leu Lys Pro Glu Asp Lys Asp Arg Arg Ile
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Leu Ile Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met
100 105 110

Gly Ala Leu Ser Phe
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<213> Homo sapiens

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<223> Repro-PC-1.0 (PC-20) "B" internal repeat (amino acid) positions 276-397

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Leu Ile Ser Leu Cys Tyr Gln Ser Thr Ile Asn Thr Leu Thr Val Val
20 25 30

Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser
35 40 45

Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser
50 55 60

Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn
65 70 75 80

Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser
85 90 95

Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val
100 105 110

Ile Gly Gln Leu Val Leu Gly Ala Ala
115 120

<210> 8
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<212> PRT
<213> rat

<220>

<221> PEPTIDE

<222> (1)..(115)

<223> synaptotagmin "B" internal repeat (amino acid positions 268-383)

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Lys Glu Glu Gln Glu Lys Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr
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Val Pro Thr Ala Gly Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn
20 25 30

Leu Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile
35 40 45

His Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile
50 55 60

Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu
65 70 75 80

Val Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu
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Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val
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Gly Tyr Asn

115

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<211> 120

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<213> rat

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<222> (1)..(120)

<223> synaptotagmin "A" internal repeat (amino acid positions 134-254)

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Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu Val Gly Ile Ile Gln
20 25 30

Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr
35 40 45

Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Phe Glu Thr Lys
50 55 60

Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu Gln Phe Thr Phe
65 70 75 80

Lys Val Pro Tyr Ser Glu Leu Gly Lys Thr Leu Val Met Ala Val
85 90 95

Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Phe Lys
100 105 110

Val Pro Met Asn Thr Val Asp Phe
115 120

<210> 10

<211> 113

<212> PRT

<213> Homo sapiens

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acid positions 150-263)

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Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro
20 25 30

Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr
35 40 45

Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys
50 55 60

Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro
65 70 75 80

Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe
85 90 95

Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu
100 105 110

Ser

<210> 11
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<223> residue 2=Asp, Glu, Ala, Ser or Thr

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<213> Homo sapiens

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<210> 15
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<212> PRT
<213> Homo sapiens

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Cys, Gly, Asp or Glu

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<223> residue 9=Lys, Arg or Tyr

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<223> residues 1, 3-8=unknown

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Cys, Gly, Asp or Glu

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Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln
20 25 30

<210> 22

<211> 34

<212> PRT

<213> Homo sapiens

<400> 22

Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val Leu
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Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys Phe
20 25 30

Gly Ala

<210> 23

<211> 25

<212> PRT

<213> Homo sapiens

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20 25

<210> 24

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<212> PRT

<213> Homo sapiens

<400> 24

Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr
1 5 10 15

Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr

20

25

30

Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp
35 40 45

Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu
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<400> 25
Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu Met Asn
1 5 10 15

Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu
20 25 30

Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
35 40 45

<210> 26
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<213> Homo sapiens

<400> 26
Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu
1 5 10 15

Val Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu
20 25 30

<210> 27
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<212> PRT
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<220>
<223> residue 5=Val or Ile

<400> 27

Ser Asp Pro Tyr Xaa Lys

1

5